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repeatt Nat. State Nat. State Nat. State Nat. State Nat. State Nat. Nat. Nat. Nat. Nat. Nat. Nat. Nat.	SEQUENCE SEQUENCE TISSUE=Fe MEDLINE=9 Uren A.G. "Cloning function- receptor- proc. Nat [4] STRUCTURE MEDLINE=9 Hidds M.G	SEQUENCE PROM TISSUB-Liver; MEDLINE-96149 Liston P., Rc Farahani R., "Suppression family of IAF Nature 379:34	SEQUENCE MEDLINE-S Rothe M., "The TNFF to baculd Cell 83:1	01-NOV-199 01-NOV-199 01-NOV-199 20-AUG-200 BACULOVIRA PROTEIN 2) PROTEIN 2) PROTEIN 2) BIRC3 OR A HOMO Sapie Eukaryota; Mammalia; Mammalia;		336 57. 336 57. 337 57. 440 55. 442 55. 544. 544. 544.
Tepeat. "  Tat. Struct. Biol. (  FUNCTION APOPTY  FORM AN HETEROMY  NECROSIS FACTOR  SUBCELLULAR LOCA  TISSUE SPECIFIC  TISSUE SPECIFIC  AND PANCREAS, LA  LEUKOCYTES.	TISSUE-FEETAL LIVERY TISSUE-FEETAL LIVERY TISSUE-FEETAL LIVERY TISSUE-FEETAL LIVERY MEDILINE-9209043; F TCLoning and expres TCLoning and expres function to inhibit function to inhibit receptor associated proc. Natl Acad. S Proc. Natl Acad. S PROCTURE BY NAMR OF MEDILINE-99332054; F HIJDDS M.G., NOTTON "Solution Structure"	SEQUENCE FROM N.A SEQUENCE FROM N.A TISSUE LIVER; MEDLINE 96149249; Liston P., Roy N. Farahani R., McLe "Suppression of a family of IAP gen Mature 379:349-35	FROM 961281 9an Pan 72-TRA Oviral 1243-1	yv-1997 (Rel. 35 yv-1997 (Rel. 35 JG-2001 (Rel. 46 LOVIRAL IAP REPE EIN 2) (IAP HOWE EIN 2) (IAP HOWE GR APIZ OR IAP sapiens (Human) ryota; Metazoa; zila; Eutheria; zila; Eutheria;	man Q16516;	55 118 118 118 118 118 118
5:648-651() DTIC SUPPRIOTIC SUPPRIOR ASSOCIATED COMPLIATION: CYTHOLOGY OF ABUSED OF ABSED		PubMed-8, Tamai K an M., Ik poptosis es."; 3(1996).	N.A. 127; PubMed-8548810; MG., Henzel W.J., Ayres T.M., Goeddel AF signaling complex contains two novel l inhibitor of apoptosis proteins."; 1252(1995).	35, 36, 40, REPEAT 2) (HJ 10, 10, 10, 10, 10, 10, 10, 10, 10, 10,	STANDARD;	7 556 5 156 5 555 6 65 0 65 8 1536 8 1536 8 249 5 249 5 1170 5 1170
	r; PubMed=8643514; PubMed=8643514; h M., Hawkins C.J., ession of apoptosis it apoptosis and/or it apoptosis. Sandori se factors.", Sci U.S.A. 93:497 OF 266-363. PubMed=10404221; PubMed=1040424; PubMed=104044; PubMed=104044; PubMed=104044; PubMed=104044; PubMed=104044; PubMed=10404; PubMe			5, Created) 5, Last sequence update) 6, Last sequence update) 2AT-CONTAINING PROTEIN 3 ((HIAP-2) (C-IAP1) (TNFR2-T) (OLOG B). P2 OR MIHB. 1. Chordata; Craniata; Verte primates; Catarrhini; Hom	R A	1 NUMB 1 80DP 1 HYDL 1 POIL 1 MTB 1 SIN3 1 EM6_ 1 BIR1 1 LAP2 1 CAF1 1 TSP1 1 TSP1
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BIR 1 / 1 / 1 / 1 / 1 / 1 / 1 / 1 / 1 / 1 /	K.L., bitory tumor 8(1996)	ovre C., Baird S Mackenzie A., K Hilan cells by N	T.M., Goe ns two no oteins.";	ite) date] N 3 (INHIBIT NR2-TRAF SIG PR2-TRAF SIG Vertebrata; Hominidae;	AA.	
REGIO (TRAF1 CRUITED CRUITED CRUITED CRUITED PHERAL	aux D. rotein ecrosi	S., Cherto Korneluk F NAIP and a	Goeddel D.V.; novel proteins	OR NAI		P16554 P36639 Q05355 Q0327287 P227287 P227373 P41134 P41134 P418856 Q28178
ION INTERACTS I AND TRAF2) TO ED TO THE TUMOR F TISSUES. TESTIS, OVARY, L BLOOD	ologs ctor	Cherton-Horvat eluk R.G.; and a related	ins	OR OF APOPTOSIS		
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Result No.

Score

Query
Match Length

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Description

100.0 100.0 98.0 95.6 95.6 63.1

BIR3 HUMAN
BIR\_CHICK
PIAP\_DIG
BIR2\_HUMAN
BIR3\_MOUSE
BIR2\_MOUSE
BIR6\_MOUSE
BIR6\_GTC
BIR6\_MOUSE
BIR6\_GTC
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013490 homo sapien 090660 gallus gall 062640 sus scrofa 213489 homo sapien 262210 mus musculu 141477 orgyla pseu 091146 mus musculu 09116 homo sapien 213075 homo sapien 213170 homo sap

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

100059

100059 seqs, 36664827 residues

Title: Perfect score:

US-08-569-749-9 295

PEQLASAGEYYVGRNDDVKC.....CWESGDDPWVEHAKWFPRCE

Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 OM protein

protein search, using

sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

January 7, 2002, 16:05:25;

Search time 77.81 Seconds (without alignments) 22.618 Million cell updates/sec

on:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summeries

Database :

SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULY 2
BIR_CHICK
ID BIR_CHICK
AC 090660;
DT 01-NOV-1997 (1)
DT 20-AUG-2001 (1)
DE INHIBITOR OF /
DE PROTEIN).
CN ITA.
OS Gallus gallus
OC AICHOSAUTIA;
OC AICHOSAUTIA;
OC AICHOSAUTIA;
OC MUBI_TAXID=90.
RN [1]
RN SEQUENCE FROM
RC TISSUE-Spleen;
RY "ITA, a verte)
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Interpro; IPR001315; CARD.
Interpro; IPR001315; CARD.
Interpro; IPR001315; CARD.
Interpro; IPR001341; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF00619; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM001184; RING; 1.
SMART; SM001184; RING; 1.
SMART; SM001184; RING; 1.
SMART; SM001184; REPEAT_2; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS0143; BIR_REPEAT_2; 3.
PROSITE; PS0143; BIR_REPEAT; 3.
APOPUSATE; PS0143; BIR_REPEAT_2; BIR_REPEAT_2;
APOPUSATE; PS0143; BIR_REPEAT_2;
APOPUSATE; PS0143; BIR_REPEAT_2;
APOPUSATE; PS0143; BIR_REPEAT_2;
APOPUSATE; PS0143; BIR_REPE
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REPEAT
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DOMAIN
N.FING
CONFLICT
CO
SEQUENCE FROM N.A.
TISSUE-Spleen;
MEDLINE-97101112; PubMed-8945639;
MEDLINE-97101112; PubMed-8945639;
Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal Digby M.R. a vertebrate homologue of IAP that is expressed in T
                                                                                                                                                                                                                                                 Tra.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Calliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L49431; AAC41942.1; -.
EMBL; Q45879; AAC50372.1; -.
EMBL; U37547; AAC50508.1; -.
PDB; 1QBH; 20-0CT-99.
MIM; 601721; -.
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                                                                                                                                                                                                             NCBI_TaxID=9031;
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SIMILARITY: CONTAINS 3 BIR REPEATS.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEQLASAGEYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 334
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1 Similarity 100.
48: Conservative
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update
F APOPTOSIS PROTEIN (IAP) (INHIB
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BIR 3.
BIR 3.
CARD.
RING-TYPE.
S > P (IN REF. 2).
C -> G (IN REF. 2).
C -> G (IN REF. 2).
C -> W (IN REF. 2).
L -> W (IN REF. 2).
L -> W (IN REF. 2).
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Pred. No. 4.4e-29;
; Mismatches 0;
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RESULT 3
PIAP_PIG
ID PIAP_PIG
AC 062640;
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L DNA CGLI BIOL 15:981-988(1996).

C -!- FUNCTION: APOPYOTIC SUPPRESSOR (BY SIMILARITY).

C -!- FUNCTION: APOPYOTIC SUPPRESSOR (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.

CC -!- TISSUE SPECIFICITY: CELLS OF THE TLYMPHOCYTE LINEAGE. FOUND IN COPTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.

CC -!- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.

CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.

CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.

CC -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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Matches 46
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InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PP00653; BIR; 3.
Pfam; PP00619; Zf-C3HC4; 1.
SMARR; SM00238; BIR; 3.
SMARR; SM00114; CARD; 1.
SMARR; SM00114; CARD; 1.
SMARR; SM00114; RING; 1
SMARR; SM00134; RING; 1
SMARR; SM00134; RING; 1
SMARR; SM00134; RING; 1
SMARR; SM00134; CARD; 1.
SMARR; SM00144; CARD; 1.
SMARR; SM00184; RING; 1
PR0SITE; PS0143; BIR, REPEAT_2; 3.
PR0SITE; PS0143; BIR, REPEAT_2; 3.
PR0SITE; PS0143; BIR, REPEAT_2; 3.
PR0SITE; PS00143; BIR, REPEAT_3; 3.
                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;
[1]
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ZN_FING
SEQUENCE
MEDLINE-98162622; PubMed-9501011;
Stehlik C., de Martin R., Binder B.R., Lipp J.;
"Cytokine induced expression of porcine inhibitor of
protein (iap) family member is regulated by NF-kappa
Biochem, Biophys, Res. Commun. 243:827-832(1998).
:- SIMILARITY: BELONGS TO THE IAP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
20-AuG-2001 (Rel. 40, Last annotation
putarive inhibitor of apoptosis.
PIAP.
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                                                                                                                                                                                        TISSUE-Aorta;
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176
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329 B
598 R
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BIR 2.
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RING-TYPE.
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InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 2.
SMART; SM00184; CARD; 1.
SMART; SM00184; CARD; 1.
SMART; SM00184; CARD; 1.
SMART; SM00184; CARD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIR2_HUMAN STANDARD; PRT; 604 AA.

Q13489; Q16628; Q9UP46;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BACULOVIRAL IAP REPERAT-CONYALINING PROTEIN 1 (INHIBITOR OF APOPTOSIS PROTEIN 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF SIGNALING COMPLEX PROTEIN 1) (IAP HOMOLOG C).
BIRC2 OR APPI OR IAPI OR MIHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. PUBMEd*8548810;
MEDLINE*96128127; PubMed*8548810;
ROTHe M., Pan M. G., Henzel W.J., Ayres T.M., Goeddel D.V.;
"The TNFR2-TRAF signaling complex contains two novel proteins to baculoviral inhibitor of apoptosis proteins.";
Cell 83:1243-1252(1995).
MEDLINE-96149249; PubMed-8552191;
Liston P., Roy N., Tamai K., Lefebvre C., Baird
Farahani R., McLean M., Ikeda J., Mackenzie A.,
"Suppression of apoptosis in mammalian cells by
family of IAP genes.";
Nature 379:349-353(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAMOH
                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis;
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 PEQLASAGEYYMGHSDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PEQLASAGEYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 95.6%;
1 Similarity 93.8%;
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS01282; BIR_REPEAT_1; PS50143; BIR_REPEAT_2; PS50209; CARD; 1.
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311
358
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BIR 2.
RING-TYPE.
RING-TYPE.
W; EB2268FA9A6190A4 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                               Korneluk
NAIP and
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                                                                               related
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BLOOD 93:3418-3431(1999).

C -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACT.

C HITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAFI AND TRAF FORM AN HETEROMERIC COMPLEX, MHICH IS THEN RECRUITED TO THE NECROSIS FACTOR RECEPTOR 2 (TNFT2).

C -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

C -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LYMPHOID TISSUES, THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES, INCLUDING SPELEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.

C -!- SIMILARITY: CONTAINS 3 BIR REPEATS.

C -!- SIMILARITY: CONTAINS 1 RIMG-TYPE ZINC FINGER.
                                                                                                                                                                                                                    Interpro; IPR001370; BIR.
Interpro; IPR001315; CARD.
Interpro; IPR001315; CARD.
Interpro; IPR001841; Znf_ring
Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD, 1.
Pfam; PF00619; Zf-C3IC4; 1.
Pfam; PF00619; Zf-C3IC4; 1.
SMART; SM00218; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; I.
PROSITE; PS01282; BIR_REPEAT;
                                                                                                                                                                                                                                                                                                                                                    EMBL; L49432; AAC41943.1; ...
EMBL; U345878; AAC50371.1; ...
EMBL; U37465; AAC50507.1; ...
EMBL; AF070674; AAC83232.1; ...
MIM; 601712; ...
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_r1n9.
PF670; PR006632; ENF_110.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
REPEAT
REMEAT
DOMAIN
ZN_FING
CONFLICT
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Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor-alpha in including inhibi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-99252096; PubMed=10233894; Horrevoets A.J., Fontijn R.D., van ten Cate J.W., Pannekoek H.; "Vascular endothelial genes that ar factor-alpha in vitro are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-99252096;
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 29
169
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   AA;
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BIR_REPEAT_2;
CARD; 1.
                  96
235
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        PREPEAT:

BIR 1.

BIR 2.

BIR 3.

CARD.

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K -> P (IN
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     CRC64;
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AND TRAF2) TO
TO THE TUMOR
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RC TISSUE-Skeletal muscle;

RC TISSUE-Skeletal muscle;

RX MEDLINE-98110590; PubMed-9441758;

RX MEDLINE-98110590; PubMed-9441758;

RX MEDLINE-98110590; Pomp W.G., Xuan J.Y., Korneluk R.G.;

RT Genomic characterization of the mouse inhibitor of apoptosis protein

RT Genomics 46:495-503(1997).

CC -1 FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS

CC WITH TWE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAP1 AND TRAP2) TO

CC HORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC HORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC HORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

CC FISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,

CC FISSUELLARITY: DELONGS TO THE IAP FAMILY.

CC FISHILLARITY: CONTAINS 3 BIR REPEAUS.

CC FISHILLARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

CC FISHILLARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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Best Local S
Matches 45
EMBL: L4943; AAC42078.1; -.
EMBL: U88909; AAC53532.1; -.
MCD: MCI:1197009; BIRC.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF006619; CARD, 1.
Pfam; PF00619; Zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00244; CARD, 1.
SMART; SM00114; CARD, 1.
PROSITE; PS01282; BIR_REPEAT_1; 3
PROSITE; PS01282; BIR_REPEAT_2; 3
PROSITE; PS01282; CARD; 1.
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G02210; OO8864;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS BIRGJ OR APIZ OR IAP2), MIAP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee1sb-sib.ch).
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MEDLLINE-96128127; PubMed-8548810;
Rothe M., Pan M. G., Henzel W.J., Ayres T.M., Goeddel D.V.;
"The TNFR2-TRAP signaling complex contains two novel proteins related to baculovital inhibitor of apoptosis proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 83:1243-1252(1995).
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Similarity 93.6
45; Conservative
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Pred. No. 1.7e-27;
2; Mismatches 1
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Best Local S
Matches 45
                                                                                          EMBL; U88908; AAC53531.1; ...
MCD; MGI:1197007; Birc2.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF00659; CARD; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUB-Skeletal muscle;
MEDLINE-98110590; PubMed-9441758;
MEDLINE-98110590; PubMed-9441758;
MEDLINE-98110590; PubMed-9441758;
MEDLINE-98110590; PubMed-9441758;
MEDLINE-Skeletal muscle;
MEDLINE-Skeletal mu
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01-NOV-1997 (Rel. 35, Last sequence update)
10-NOV-1997 (Rel. 35, Last sequence update)
20-NUG-2001 (Rel. 40, Last annotation update)
BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 2 (INHIBITOR OF APOPTOSIS PROTEIN 1) (MIAP-1).
BIRC2 OR APII OR IAPI.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis;
REPEAT
REPEAT
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DOMAIN
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CONFLICT
SEQUENCE
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PROSITE; PS01282; BIR_REPEAT_1; PROSITE; PS50143; BIR_REPEAT_2; PROSITE; PS50209; CARD; 1.
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008863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 PEQLASAGEYYVDRNDDVKCFCCDGGLRCWEPGDDPWIEHAKWFPRCE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDDWVEHAKWFPRCE 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
177
262
447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÅA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Repeat.

13 BIR 1.

243 BIR 2.

329 BIR 3.

533 CARD.

749 RING-TYPE.

E -> K (IN REF. 2).

508969D93C6C610D CRC64;

10-27;

10-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S REGION INTERACTS (TRAF1 AND TRAF2) TO CRUITED TO THE TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indels
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XFFFFFX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                 InterPro; IPR001370; BIR.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PP00653; BIR; 2.
Pfam; PP00097; Zf C3HC4; 1.
SMART; SM00184; BIR; 2.
SMART; SM00184; RING; 1.
PROSITE: PS01787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                          polyhedrosis virus genome.";

Virology 229:381-399(1997).

-! FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS

-! FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS.

-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis;
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. PubMed-8139034; MEDLINE-94187094; PubMed-8139034; MEDLINE-94187094; PubMed-8139034; Birnbaum M.J., Clem R.J., Miller L.K.; Birnbaum M.J., Clem R.J., Miller L.K.; An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polypeptide with Cys/His sequence motifs."; J. Virol. 68:2521-2528(1994).
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PROSITE: PS01282; BIR_REPEAT_1; 2.
PROSITE: PS50143; BIR_REPEAT_2; 2.
Apoptosis: Inc finger; Repeat 1.
REPEAT 18 64 PBIR 2.
ZN_FING 221 255 RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no
Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                            EMBL; L22564; AAB02610.1;
EMBL; U75930; AAC59034.1;
                                                                                                                                                                                                                                                                                                                                                                                                                 Ahrens C.H., Russell R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=97271300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APOPTOSIS IN
IAP3 OR IAP
                                                                                                                                                                                                                                                                                                                                                                           "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                       Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AP3_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
s; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 (Rel. 32, Created)
95 (Rel. 32, Last sequence update)
01 (Rel. 40, Last annotation update)
INHIBITOR 3 (IAP-3).
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27
167
253
444
553
600 A
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                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9126251;
ell R.R., Funk C.J.,
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587
67198
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BIR 2.
BIR 3.
CARD.
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: AD7F73E6849317D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                 Evans J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; L
1.2e-26;
les 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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BIRF_MOUSE
 Query Match
Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                      EMBL; AF242431; AAF82751.1; -.
EMBL; 066327; AAC52975.1; -.
MGD; MG1:1298222; Birclf.
Interpro; IPR001370; BIR.
Pfam; PF00653; BIR; 3
SMART; SM00238; BIR; 3
SMART; SM00238; BIR, REPEAT_1; 2
PROSITE; PS50143; BIR_REPEAT_2; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIRE_MOUSE STANDARD; PRT; 1403 AA. 093/IB6; P81704; C091/22; C009121; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN IF INHIBITORY PROTEIN 6.

BIRCIF OR NAIP5 OR NAIP-RS4.
                                                                             REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.;
"The mouse region syntenic for human spinal muscular atrophy lies within the Lgnl critical interval and contains multiple copies of exon 5.";
Genomics 38:405-417(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-2041474; PubMed-10958627; MEDLINE-2041474; PubMed-10958627; Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich "Genomic sequence analysis of the mouse Naip gene array."; Genome Res. 10:1095-1102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 82-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97131520; PubMed-8975718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 3 BIR REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·! - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129
                                                                                                                                           Apoptosis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEELAEAGFFYTGQGDKTRCFCCDGGLKDWEPDDAPWQQHARWYDRCE
ch 63.4%;
l Similarity 60.4%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 60.4
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREVENTS
                                                                               AA;
                                                                           BIR_REPEAT_1; 2.
BIR_REPEAT_2; 3.
; Multigene family.
127
BIR 1.
227
BIR 2.
345
BIR 3.
345
BIR 3.
4; 159823 MW; 9D49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30076 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 198; DB 1;
Pred. No. 1.9e~17;
8; Mismatches 11
Score 187; DB 1; Length 1403; Pred. No. 2e-15; 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DF89175FDE85A708 CRC64;
                                                                               9D4912503358C4E9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                               CRC64;
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178

PEQLASAGFYYYGRNDDVKCFCCCDGGLRCWESGDDPWVEHAKWFPRCE PRALSAAGFVFTGKRDTVQCfSCGGSLGNWEEGDDPWKEHAKWFPKCE 225

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RESULT 10
BIRA_MOUSE
              SAFFFFFF SSSSS
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 16 (INHIBITORY PROTEIN 7).
BIRCIG OR NAIP?
DIRA_MOUSE STANDARD; PRT; 1403 AA.
090WK5; 09R017; 09JIB5;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1A (NEURONAL APOPTOSIS INHIBITORY PROTEIN 1).
BIRCLA OR NAIP1 OR NAIP.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
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MEDLINE=20414747; PubMed=10958627;

MEDLINE=20414747; PubMed=10958627;

Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.

"Genomic sequence analysis of the mouse Naip gene array.";

"Genome Res. 10:1095-1102(2000).

"I- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY

"TOWN" OF TAXABLE PROPERTY OF TAXABLE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF242433; AAF82749.1; -. MGD; MGI:1889256; Bircig. Interpro; IPR001370; Bir. Pfam: PF00653; Bir; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentla;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01282; BIR_REPEAT_1; 2.
PS50143; BIR_REPEAT_2; 3.
PS50143; BIR_REPEAT_2; 3.
PS50143; BIR_REPEAT_1; 3.
PS50145; BIR 1.
PS50127
PS60127
PS6012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.1%;
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Pred. No. 2.6e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
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RESULT 11
BIRE_MOUSE
ID BIRE_M
AC Q9R016
DT 20-AUG
DT 20-AUG
DT 20-AUG
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Best Local Similarity 60.4
Matches 29; Conservative
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EMBL; AF735491; AAD56763.1; -.
EMBL; AF724421; AAF82752.1; -.
MGD; MGI:1298223; Bircla.
Interpro; IPR001370; Bir.
Pfam; PF00653; Bir; 3.
SMART; SM00238; Bir; 3.
PROSITE; PS011282; Bir_REPEAT_1; 1
PROSITE; PS011282; Bir_REPEAT_2; 3
PROSITE; PS01143; Bir_REPEAT_2; 3
PROSITE; PS0143; Bir_REPEAT_2; 3
PROSITE; PS0143; Bir_REPEAT_2; 3
PROSITE; PS0143; Bir_REPEAT_3; 3
PROSITE; PS0143; Bir_REPEAT_2; 3
PROSITE; PS0143; Bir_REPEAT_3; 3
PROSITE; PS0143; Bir_REPEAT_1; 1
PROSITE; PS0143; Bir_REPEAT_1; Bir_REPEAT_1; 1
PROSITE; PS0143; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEAT_1; Bir_REPEA
BIRE_MOUSE STANDARD; PRT; 1403 AA 09R016; 09R016; 09R029; P81703; 009122; 009121; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
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MEDLINE-99431676; PubMed-10501978;

Huang S., Scharf J.M., Growney J.D., Endrizzi

"The mouse Naip gene cluster on Chromosome 13
functional transcripts,";

Mamm. Genome 10:1032-1035(1999).
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SEQUENCE FROM N.A.

MEDILINE-20414747; PubMed-10958627;

MEDILINE-2041747; PubMed-10958627;

MEDILINE-2041747; PubMed-10958627;

"Genomic sequence analysis of the mouse Naip gene array.";

Genomic sequence analysis of the mouse Naip gene array.";

Genome Res. 10:1095-1102(2000).
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-I- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED
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Yarashi Z., Korneluk R.G., MacKenzie A.E.;

Yarashi Z., Korneluk R.G., MacKenzie A.E.;

"Cloning and characterization of the multiple copies of the murine homologue of NAIP (neuronal apoptosis inhibitory protein).";

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: CONTAINS 3 BIR REPEATS.
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T_2; 3.
T_2; 3.
T_2; 3.
T_2; 3.
Effective and the second a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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APOPTOSÍS;
REPEAT
REPEAT
CONFLICT
CONFL
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InterPro. IPR001370; BIR,
Pfam; PF00653; BIR; 3.
SMART; SM00238; BIR; 3.
PROSITE; PS01282; BIR, REPEJ
PROSITE; PS50143; BIR_REPEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97131520; PubMed-8975718; Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H., Scharf J.M., Dietrich W.F.; Kunkel L.M., Dietrich W.F.; The mouse region syntenic for human spinal muscular atrophy lies within the Lgnl critical interval and contains multiple copies of exon 5."; Genomics 38:405-417(1996).
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INHIBITORY PROTEIN 5).
BIRCLE OR NAIP5 OR NAIF-RS3.
Mus musculus (Mouse).
Bukaryota, Netazoa; Chordata; Cran
Mammalia; Eutheria; Rodentia; Sciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99417674; PubMed-10486205;
Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
Kunkel L.M., Miller W., Dietrich W.F.;
"Comparative sequence analysis of the mouse and human Lgnl
interval.";
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Huang S., Scharf J.M., Growney J.D., Endrizzi
"The mouse Naip gene cluster on Chromosome 13
functional transcripts.";
Mamm. Genome 10:1032-1035(1999).
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EMBL;
MGD; I
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AF131205; AAD56760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
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BIR_REPEAT_2;
t: Multigene fam
                               127
227
345
49
144
242
242
516
521
533
538
538
1092
11242
1242
      159695
   Craniata; Vertebrata; Euteleostomí; Sciurognathi; Muridae; Murinae; Mus
      B27F645043BCEC42
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                               REET .
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encodes several distinct
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      CRC64;
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RESULT 12
BIRB_MOUSE STANDARD; PRT: 1447
ID BIRB_MOUSE (OP9124;
D7 20-NUG-2001 (Rel. 40, Created)
D7 20-NUG-2001 (Rel. 40, Last sequence updat
D8 20-NUG-2001 (Rel. 40, Last sequence updat
D8 20-NUG-2001 (Rel. 40, Last sequence
D8 20-NUG-2001 (Rel. 40, Last sequence
D8 20-NUG-2001 (Rel. 40, Last sequence
D8 20-NUG-2001 (Rel. 40, Last sequence)
D8 BIRCIB OR NAIP2 CR NAIP-RS6.

OC Mus musculus (Mouse).

OC Musc
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Best Local
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Genomics 38:405-417(1996).
1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED SIGNALS.
11- SIMILARITY: CONTAINS 3 BIR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.;
"The mouse region systemic for human spinal muscular atrophy liwithin the Lgnl critical interval and contains multiple copies exon 5.";
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MEDLINE-99431676; PubMed-10501978;
Huang S., Scharf J.M., Growney J.D., Endrix
"The mouse Naip gene cluster on Chromosome
functional transcripts.";
Mamm. Genome 10:1032-1035(1999).
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Endrizzi M., Huang S., Scharf J.M., Kelter A.R.,
Kunkel L.M., Miller W., Dietrich W.F.;
"Comparative sequence analysis of the mouse and
interval."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE-99315342; PubMed-10384056; Yaraghi Z., Diez E., Gros P., MacKenzie A.; Yaraghi Z., Diez E., Gros P., MacKenzie A.; "cDNA cloning and the 5'genomic organization gene for murine Legionella resistance."; Mamm. Genome 10:761-763(1999).
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Pred. No. 2
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN 1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelter A.R., Wirth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endrizzi M.G., Dietrich W.F.;
nosome 13 encodes several distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human Lgnl/SMA
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; Murinae; Mus
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29; AAC52977.1; -.

21PO 198026; B1rclb.

24Pro 1PRO01370; B1R.

24APT: SHER.

25APT: PS001282; B1R.

25APT: PS00143; B1R.REPEAT_1; 2.

25APT: PS00143; B1R.REPEAT_2; 3.

27 B1R 1.

28 PROSITE: PS00143; B1R.REPEAT_2; 3.

27 B1R 2.

28 PROSITE: PS00143; B1R.REPEAT_2; 3.

27 B1R 2.

28 B1R 3.

29 B1R 2.

21 B1R 2.

27 B1R 2.

28 B1R 3.

29 CIN REF. 3).

20 CIN REF. 3).

21 CIT 403 A03 L -> F(IN REF. 3).

21 1125 F -> G(IN REF. 3).

21 1126 F -> G(IN REF. 3).

21 1127 F -> G(IN REF. 3).

21 1127 F -> G(IN REF. 3).

21 1137 S -> G(IN REF. 3).

22 T -> A(IN REF. 3).

23 1143 F -> C(IN REF. 3).

24 1157 S -> G(IN REF. 3).

25 C(IN REF. 3).

26 C(IN REF. 3).

27 128 SCORE 183; D8 1; Lered. No. 6.4e-15.

Mismatches
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Best Local S
Matches 29
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on tis use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                             Kang W.K., Crook N.E., Winstanley D., O'Reilly D.R.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN
-PREVENTING VIRAL STIMULATION OF APOPTOSIS.
-I-SIMILARITY: CONTAINS 3 BIR REPEATS.
-I-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                       MEDLINE-93188168; PubMed-8445726;
Crook N.E., Clem R.J., Miller L.K.;
"An apoptosis-inhibiting baculovirus gene with a zinc finger-like
motif.";
J. Virol. 67:2168-2174(1993),
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAP_GVCP STANDARD: P41436;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence 20-AUG-2001 (Rel. 40, Last and APOPTOSIS INHIBITOR IAP.
                                                                                                                                                                                                                                                                                                                                                                                               Cydia pomonella granulosis virus (CpGV) (Cydia pomonella granulovirus).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae: Gran
                                                                                                                                                                                                              STRAIN-MEXICAN;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses,
NCBI_TaxID=28289;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRVLSAAGFVFTGKRDTVQCFSCGGCLGNWEEGDDPWKEHAKWFPKCE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                                                                                                                                                                                                                                                                               RNA stage; Baculoviridae; Granulovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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RESULT 14
BIR1_HUMAN
ID BIR1_H BIR1_H
AC G13075
AC MARMMALI
CON MARMMALI
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RA FARAH
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                   MEDIJUR-9813755; PubMed-9503025; Chen Q., Baird S.D., Mahadevan M., Besner-Yuan J.Y., Kang X., Lefebvre C., Ikeda J. MacKenzie A.E.; "Sequence of a 131-kb region of 5q13.1 con atrophy candidate genes SMN and NAIP."; Genomics 48:121-127(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L05494; ANA43835.1; ...
EMBL; L05496; AAB39098.1; ...
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PP00539; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00238; RIR; 1.
PR0SITE; PS01282; BIR, REPEAT_1; 2
PR0SITE; PS01282; BIR_REPEAT_2; 2
PR0SITE; PS0143; BIR_REPEAT_2; 2
Apoptosis; Zinc-finger; Repeat.
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

TISSUE-Fetal brain:

MEDLINE-95112344; Pubmed-7813013;

ROY N., Mahadevan M.S., McLean M., Shutler G., Yaraghi Z.,

Farahini R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,

Farahini M., Aubry H., Tamai K., Guan X., Toannou P., Crawford T.O.,

de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;

"The gene for neuronal apoptosis inhibitory protein is partially

deleted in individuals with spinal muscular atrophy.";

Cell 80:167-178(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIR1_HUMAN STANDARD; PRT: 1403 AA. 013075; 013730; 099796; 075857; 01-NOV-1997 (Rel. 35, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
ZN_FING
SEQUENCE
                                                                                                                        SEQUENCE OF 386-623 FROM N.A. der Steege G., Draaijers T.G., Anzevino R., Velona I., Brahe (Buys C.H.C.M.; Submitted (MAY-1995) to the EMI
SEQUENCE OF 222-1403 FROM N.A. Jones K., Graves T., McPherson J.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INHIBITORY PROTEIN).
BIRC1 OR NAIP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
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228
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.7%;
nilarity 59.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 BIR 1.
175 BIR 2.
252 RING-TYPE.
31290 MW; 84605448869CAD60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 182; DB
; Pred. No. 1.8e
6; Mismatches
                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                         C., Scheffer H., van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    5q13.1 containing the spinal muscular NAIP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NN
                                                                                                                                                                                                                                                                                                                                                                      Besner-Johnston A., Farahani R.,
[keda J.~E., Korneluk R.G.,
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알
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..8e-15;
les 13;
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                            databases
                                                                                                                              databases
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Ommen (
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Best Local Similarity 60.4
Matches 29; Conservative
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                                                                                                                                              _MOUSE
060989; 008865;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
BACULOVIRAL LAP REPEAT-CONTAINING PROT
PROTEIN 3) (X-LINKED INHIBITOR OF APOP
(IAP HOMOLOG A) (MIAP3) (MIAP-3).
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CONFLICT
CONFLICT
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CONFLICT
SEQUENCE
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PROSITE;
PROSITE;
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EMBL; U80011; AAC52047.1; -.
EMBL; U21913; AAA64504.1; -.
EMBL; AC005031; AAC62261.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee1sb-sib.ch).
                                                                                                                              BIR4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                        178
                                                                                                                                                                                                                  SPINAL CORD.

SPINAL CORD.

SPINAL CORD.

SPINAL CORD.

INDISASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN INDISASE: MUTATED AS TYPE 1). SMAS INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMATYPE AS TYPE 1)

ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1

(WERNIG-HOFFMANN DISBASE), TYPE II (INTERNEDIATE FORM), AND TYPE II (WOHLFART-KUGELBERG-WELANDER DISBASE) BASED UPON THE AGE OF ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 3 BIR REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTO: IPR001370; BIR.
PF00653; BIR; 3.
PF000238; BIR; 3.
PS01282; BIR_REPEAT_1;
PS01283; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFICITY: EXPRESSED IN MOTOR NEURONS,
                                                                                                                                                                                                                                                                                                                                                                                   159
278
228
222
386
535
1228
1403
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227
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387
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                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                           60.3%;
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BIR 2.
BIR 3.
FI > YR (IN REF. 4).
FW > YR (IN REF. 3).
FY > V (IN REF. 3).
FY > H (IN REF. 3).
FY > H (IN REF. 4).
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                                                                                                                                                                                                                                                                                       Score 178; DB
Pred. No. 2.6e
5; Mismatches
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                                                                                                                              PRT;
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                ce update)
tion update)
PROTEIN 4 (INHIBITOR OF APOPTOSIS
APOPTOSIS PROTEIN) (X-LINKED IAP)
                                                                                                                              496
                                                                                                                                                                                                                                                                                         DB 1; L
.6e-14;
es 14;
                                                                                                                              B
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NAIP and a related
                                                                                                                                                                                                                                                                                           Indels
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LESSER EXTENT IN
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Best Local S
Matches 28
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EMBL; U86899; AAB58356.1; -.
MGD; MG1:107572; Birc4.
InterPro; IPR001370; BIR.
InterPro; IPR001370; BIR,
InterPro; IPR001370; BIR; 3.
Pfam; PF00653; BIR; 3.
Pfam; PF00053; BIR; 3.
SMART; SM00238; BIR; 3.
SMART; SM00238; BIR; 3.
SMART; SM00238; BIR; 3.
                                                                                        REPEAT
ZN_FING
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6 X CBA; TISSUE-Liver;
WEDLINE-$620843; pubMed-$643514;
Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., V.
"Cloning and expression of apoptosis inhibitory no function to inhibit apoptosis and/or bind tumor no receptor associated factors.";
Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
                                                                                                                                                                                                                        PROSITE; PS01282; BIR_REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
Apoptosis; Zinc-finger; Repeat_2;
REPEAT 26 93
REPEAT 163 230
BIR
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Farahani R., Lefe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIRC4 OR API3 OR XIAP OR AIPA OR
                    N
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                       490
496
                                         Conservative
                                                                                                              163
264
449
208
317
317
346
368
469
                                                                                         AA.
                                                                                         56079
                                                 59.0%;
59.6%;
                                                                                          WW.
                                        6
                                                                                                  Score 174;
Pred. No. 3.
                                                                                            EC5FAE0799F2CDD8
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIHA
                                                                                                    REF. 2).
                                                  DB 1;
.1e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaux D.L.;
protein homologs that
necrosis factor
                                                          Length 496
                                                                                          CRC64;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                          0
                                         Gaps
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Job time: 1405 sec

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